GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 16, 2005, 20:10:09 ; Search time 127 Seconds
(without alignments)
15.227 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	7	8	ADI52979	Adi52979 Polysacch
2	24	100.0	11	5	ABG94362	Abg94362 Human tum
3	24	100.0	11	5	ABG80698	Abg80698 Human tum
4	24	100.0	11	8	ADI40738	Adi40738 Human TNF
5	24	100.0	14	6	ADA19860	Ada19860 TNFalpha
6	24	100.0	14	8	ADI40811	Adi40811 C-TNF-alp
7	24	100.0	16	6	ADA19837	Ada19837 TNFalpha
8	24	100.0	16	6	ADA19839	Ada19839 TNFalpha
9	24	100.0	16	6	ADA19856	Ada19856 TNFalpha
10	24	100.0	16	6	ADA19851	Ada19851 TNFalpha
11	24	100.0	16	6	ADA19833	Ada19833 TNFalpha
12	24	100.0	16	6	ADA19836	Ada19836 TNFalpha
13	24	100.0	17	6	ABR42094	Abr42094 Human tum
14	24	100.0	20	2	AAR05522	Aar05522 Tumour ne
15	24	100.0	21	2	AAR06807	Aar06807 Tumour ne
16	24	100.0	30	2	AAR05523	Aar05523 Tumour ne
17	24	100.0	30	2	AAR06804	Aar06804 Tumour ne
18	24	100.0	30	6	ADA19844	Ada19844 TNFalpha
19	24	100.0	30	6	ADA19845	Ada19845 TNFalpha
20	24	100.0	30	6	ADA19854	Ada19854 TNFalpha
21	24	100.0	30	6	ADA19847	Ada19847 TNFalpha
22	24	100.0	30	6	ADA19850	Ada19850 TNFalpha
23	24	100.0	30	6	ADA19858	Ada19858 TNFalpha
24	24	100.0	30	6	ADA19832	Ada19832 TNFalpha
25	24	100.0	30	6	ADA19827	Ada19827 TNFalpha
26	24	100.0	30	6	ADA19841	Ada19841 TNFalpha
27	24	100.0	30	7	ADK41113	Adk41113 Human tum
28	24	100.0	31	6	ADA19830	Ada19830 TNFalpha
29	24	100.0	31	6	ADA19849	Ada19849 TNFalpha
30	24	100.0	31	6	ADA19857	Ada19857 TNFalpha
31	24	100.0	31	6	ADA19838	Ada19838 TNFalpha
32	24	100.0	32	8	ABO58737	Abo58737 Human gen
33	24	100.0	35	7	ADK41079	Adk41079 Human tum
34	24	100.0	36	3	AAB38436	Aab38436 Fragment
35	24	100.0	51	4	AAE13097	Aae13097 Peptide #
36	24	100.0	51	5	AAG66035	Aag66035 Amino aci
37	24	100.0	51	8	ADL16846	Adl16846 BTL.010 p
38	24	100.0	52	8	ADJ36285	Adj36285 Self-coal
39	24	100.0	69	3	AAG01730	Aag01730 Human sec
40	24	100.0	70	5	ABP34565	Abp34565 Human cyt
41	24	100.0	87	5	ABP34953	Abp34953 Human ORF
42	24	100.0	88	4	AAU52620	Aau52620 Propionib
43	24	100.0	88	6	ABM49139	Abm49139 Propionib
44	24	100.0	102	2	AAW95352	Aaw95352 Human adu
45	24	100.0	102	7	ADA44978	Ada44978 Human pol

ALIGNMENTS

RESULT 1
ADI52979
ID ADI52979 standard; peptide; 7 AA.
XX
AC ADI52979;
XX
DT 06-MAY-2004 (first entry)
XX
DE Polysaccharide binding (PB) peptide #15.
XX
KW Drug delivery; polysaccharide binding; PB.
XX
OS Unidentified.
XX
PN US2003190364-A1.
XX
PD 09-OCT-2003.
XX
PF 01-APR-2003; 2003US-00405339.
XX
PR 01-APR-2002; 2002US-0369568P.
XX
PA (PANI/) PANITCH A.
PA (SEAL/) SEAL B.
XX
PI Panitch A, Seal B;
XX
DR WPI; 2004-069109/07.
XX
PT Composition useful for releasing therapeutic agent comprises a polymer
PT network, several polysaccharide binding polypeptides bound to the polymer
PT network and negatively charged polysaccharides bound to the polypeptides.
XX
PS Claim 9; SEQ ID NO 40; 33pp; English.
XX
CC The present invention provides compositions for drug delivery, comprising
CC a polymer network, several polysaccharide binding (PB) polypeptides and
CC negatively charged polysaccharides. The present sequence is
CC polysaccharide binding (PB) peptide.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 24; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||

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Db          1 LNRRA 5

RESULT 2
ABG94362
ID   ABG94362 standard; peptide; 11 AA.
XX
AC   ABG94362;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human tumour necrosis factor (TNF) epitope #2.
XX
KW   Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW   cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW   vaccine; infectious disease.
XX
OS   Homo sapiens.
XX
PN   WO200256905-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-IB000166.
XX
PR   19-JAN-2001; 2001US-0262379P.
PR   04-MAY-2001; 2001US-0288549P.
PR   05-OCT-2001; 2001US-0326998P.
PR   07-NOV-2001; 2001US-0331045P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI   Renner WA,  Bachmann M,  Tissot A,  Maurer P,  Lechner F,  Sebbel P;
PI   Piossek C;
XX
DR   WPI; 2002-627351/67.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PT   diseases.
XX
PS   Disclosure; Page 82; 441pp; English.
XX
CC   This invention relates to a novel ordered and repetitive antigen array
CC   used in the production of vaccines for infectious diseases. The invention
CC   also discloses a composition comprising a non-natural molecular scaffold
CC   comprising a core particle selected from a core particle of a non-natural
CC   origin and a core particle of natural origin and an organiser comprising
CC   at least one first attachment site, where the organiser is connected to
CC   the core particle by at least one covalent bond. Also disclosed is an
CC   antigen or antigenic determinant with at least one second attachment
CC   site, where the antigen or antigenic determinant is amyloid beta peptide
CC   (Abeta1-42) or its fragment and where the second attachment site is
CC   selected from an attachment site not naturally occurring with the antigen
CC   or antigenic determinant and an attachment site naturally occurring with
CC   the antigen or antigenic determinant, where the second attachment site is
CC   capable of association through at least one non-peptide bond to the first
CC   attachment site and where the antigen or antigenic determinant and the
CC   scaffold interact through the association to form an ordered and
CC   repetitive antigen array. The invention also comprises a coat protein
CC   capable of forming a capsid which comprises mutant Qbeta coat proteins
CC   having an amino acid sequence selected from five amino acid sequences
CC   fully defined in the specification. The compounds of the invention may
CC   have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC   antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC   immunisation and as a vaccine. The present sequence represents a protein
CC   sequence used to create the compositions of the invention
XX
SQ   Sequence 11 AA;

  Query Match             100.0%;  Score 24;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          5 LNRRA 9


RESULT 3
ABG80698
ID   ABG80698 standard; peptide; 11 AA.
XX
AC   ABG80698;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human tumour necrosis factor 22-32 epitope.
XX
KW   Molecular antigen array; vaccine; antigen; antimicrobial;
KW   molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW   graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW   adult respiratory distress syndrome; ARDS; Crohn's disease;
KW   allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW   Grave's disease; systemic lupus erythematosus; osteoporosis;
KW   inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW   immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW   angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy;
KW   rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW   enterokinase; cysteine-containing linker.
XX
OS   Homo sapiens.
XX
PN   WO200256907-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-IB000168.
XX
PR   19-JAN-2001; 2001US-0262379P.
PR   04-MAY-2001; 2001US-0288549P.
PR   05-OCT-2001; 2001US-0326998P.
PR   07-NOV-2001; 2001US-0331045P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA   (NOVS ) NOVARTIS PHARMA AG.
PA   (MAUR/) MAURER P.
PA   (LECH/) LECHNER F.
PA   (ORTM/) ORTMANN R.
PA   (LUEO/) LUEOEND R.
PA   (STAU/) STAUFENBIEL M.
PA   (FREY/) FREY P.
XX
PI   Maurer P,  Lechner F,  Ortmann R,  Lueoend R,  Staufenbiel M,  Frey P;
PI   Renner WA,  Bachmann M,  Tissot A,  Sebbel P,  Piossek C;
XX
DR   WPI; 2002-636514/68.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PT   diseases.
XX
PS   Disclosure; Page 82; 418pp; English.
XX
CC   The invention relates to a composition comprising: (a) a non-natural
CC   molecular scaffold comprising: (i) a core particle selected from: (1) a
CC   core particle of a non-natural origin; and (2) a core particle of natural
CC   origin; and (ii) an organiser comprising at least one first attachment
CC   site, where the organiser is connected to the core particle by at least
CC   one covalent bond; (b) an antigen or antigenic determinant with at least
CC   one second attachment site, where the antigen or antigenic determinant is
CC   amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC   attachment site is selected from: (i) an attachment site not naturally
CC   occurring with the antigen or antigenic determinant; and (ii) an
CC   attachment site naturally occurring with the antigen or antigenic
CC   determinant, where the second attachment site is capable of association
CC   through at least one non-peptide bond to the first attachment site; and
CC   where the antigen or antigenic determinant and the scaffold interact
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CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastive lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is an antigen
CC for use in the array of the invention. The antigen is modified to posses
CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
CC virus like particle or bacterial protein (the scaffold protein)
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 24; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 5 LNRRA 9

RESULT 4
ADI40738
ID ADI40738 standard; peptide; 11 AA.
XX
AC ADI40738;
XX
DT 22-APR-2004 (first entry)
XX
DE Human TNF-alpha peptide SEQ ID NO:29.
XX
KW virus-like particle; bacteriophage AP205; coat protein; cytostatic;
KW vaccine; gene therapy; cancer; allergy; asthma; TNF-alpha.
XX
OS Homo sapiens.
XX
PN WO2004007538-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-EP007572.
XX
PR 17-JUL-2002; 2002US-0396126P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofa R;
XX
DR WPI; 2004-122882/12.
XX
PT New virus-like particle, useful for preparing a composition for treating
PT or preventing a disease e.g., cancer, allergy or asthma.
XX
PS Disclosure; SEQ ID NO 29; 170pp; English.
XX
CC The present invention describes a virus-like particle (I) which
CC comprises: (a) a protein having the 131-amino acid sequence of
CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
CC or ADI40712 respectively; or (b) a mutein of the protein of (a). Also
CC described: (1) a mutein of the recombinant protein having the 131-amino
CC acid sequence; (2) a vector for producing a AP205 virus like particle
CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
CC identical to that of the sequence comprising 3635 or 3613 bp or producing
CC a recombinant protein comprising a nucleotide sequence encoding a
CC polypeptide fused to a protein; (3) a pharmaceutical composition
CC comprising the composition and a carrier; (4) a process for producing a
CC non-naturally occurring, ordered and repetitive antigen array; (5) a
CC method of treating or preventing a disease, disorder or physiologic
CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
CC (8) a method of producing the virus-like particle. (I) has cytostatic
CC activity, and can be used in vaccines, and in gene therapy. The virus-
CC like particle is useful for preparing a composition for treating or
CC preventing a disease e.g., cancer, allergy or asthma. The present
CC sequence represents a TNF-alpha peptide, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 24; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 5 LNRRA 9

RESULT 5
ADA19860
ID ADA19860 standard; peptide; 14 AA.
XX
AC ADA19860;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:34.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 22; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test

CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 24; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 7 LNRRA 11

RESULT 6
ADI40811
ID ADI40811 standard; peptide; 14 AA.
XX
AC ADI40811;
XX
DT 22-APR-2004 (first entry)
XX
DE C-TNF-alpha peptide mutant SEQ ID NO:102.
XX
KW virus-like particle; bacteriophage AP205; coat protein; cytostatic;
KW vaccine; gene therapy; cancer; allergy; asthma; TNF-alpha; mutant.
XX
OS Synthetic.
XX
PN WO2004007538-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-EP007572.
XX
PR 17-JUL-2002; 2002US-0396126P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofa R;
XX
DR WPI; 2004-122882/12.
XX
PT New virus-like particle, useful for preparing a composition for treating
PT or preventing a disease e.g., cancer, allergy or asthma.
XX
PS Disclosure; SEQ ID NO 102; 170pp; English.
XX
CC The present invention describes a virus-like particle (I) which
CC comprises: (a) a protein having the 131-amino acid sequence of
CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
CC or ADI40712 respectively; or (b) a mutein of the protein of (a). Also
CC described: (1) a mutein of the recombinant protein having the 131-amino
CC acid sequence; (2) a vector for producing a AP205 virus like particle
CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
CC identical to that of the sequence comprising 3635 or 3613 bp or producing
CC a recombinant protein comprising a nucleotide sequence encoding a
CC polypeptide fused to a protein; (3) a pharmaceutical composition
CC comprising the composition and a carrier; (4) a process for producing a
CC non-naturally occurring, ordered and repetitive antigen array; (5) a
CC method of treating or preventing a disease, disorder or physiologic
CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
CC (8) a method of producing the virus-like particle. (I) has cytostatic
CC activity, and can be used in vaccines, and in gene therapy. The virus-
CC like particle is useful for preparing a composition for treating or
CC preventing a disease e.g., cancer, allergy or asthma. The present
CC sequence represents a TNF-alpha mutant peptide, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 24; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 8 LNRRA 12

RESULT 7
ADA19837
ID ADA19837 standard; peptide; 16 AA.
XX
AC ADA19837;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:11.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 16; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules

CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||| |
Db 9 LNRRA 13

RESULT 8
ADA19839
ID ADA19839 standard; peptide; 16 AA.
XX
AC ADA19839;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:13.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 17; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||| |
Db 4 LNRRA 8

RESULT 9
ADA19856
ID ADA19856 standard; peptide; 16 AA.
XX
AC ADA19856;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:30.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;

KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 21; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||| |
Db 8 LNRRA 12

RESULT 10

ADA19851
ID ADA19851 standard; peptide; 16 AA.
XX
AC ADA19851;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:25.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 20; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the

```
CC   exemplification of the present invention.
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 24;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          2 LNRRA 6


RESULT 11
ADA19833
ID   ADA19833 standard; peptide; 16 AA.
XX
AC   ADA19833;
XX
DT   20-NOV-2003  (first entry)
XX
DE   TNFalpha receptor binding peptide SEQ ID NO:7.
XX
KW   molecular library; identification; detection; binding site;
KW   tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW   protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW   TNFalpha receptor; tumour necrosis factor alpha receptor;
KW   inflammatory disease; Crohn's disease; intestinal ulceration;
KW   intestinal irritation.
XX
OS   Synthetic.
XX
PN   EP1279962-A1.
XX
PD   29-JAN-2003.
XX
PF   27-JUL-2001; 2001EP-00202879.
XX
PR   27-JUL-2001; 2001EP-00202879.
XX
PA   (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI   Slootstra JW,  Puijk WC,  Van Dijk E;
XX
DR   WPI; 2003-259178/26.
XX
PT   Producing molecular library for identifying binding site of tumor
PT   necrosis factor-alpha, comprises providing the library with many
PT   molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS   Disclosure; Page 15; 70pp; English.
XX
CC   The present invention describes a method (M1) for producing a molecular
CC   library for identifying or detecting a binding site of tumour necrosis
CC   factor alpha (TNFalpha). (M1) comprises providing the library with
CC   several molecules, and further generating at least one of the molecules
CC   by linking a first segment to a second segment. Also described: (1) a
CC   library (I) comprising several molecules comprising at least a first and
CC   a second segment obtainable by (M1); (2) a solid support (II) comprising
CC   (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC   identifiable or obtainable by using (I); and (4) determining (M2) a
CC   minimally essential motif for a binding site, by generating a library of
CC   test molecules, determining the binding activity of a binding molecule
CC   with the test molecules, calculating the average binding activity of test
CC   molecules present in the library comprising a certain motif, and
CC   determining a motif with a high average binding activity of test
CC   molecules comprising the motif. (M1) is useful for producing a molecular
CC   library for identifying or detecting a binding site of TNFalpha. (I) is
CC   useful for screening for a binding site of TNFalpha capable of
CC   interacting with a binding molecule, by screening a library with at least
CC   one potential binding molecule and detecting binding between a member of
CC   the library and the potential binding molecule. The binding molecule
CC   comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC   binding site. (I) and (II) are useful for identifying or obtaining a
CC   synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC   molecule capable of binding to a binding site of hTNFalpha. (III) is
CC   useful for interfering with or effecting binding to a binding molecule of
CC   hTNFalpha. The molecular libraries produced by (M1) are useful for
CC   detecting or screening for discontinuous binding sites, in particular in
CC   relation to binding molecule-ligand interactions such as for e.g. protein
CC   -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC   interactions. The identified peptide constructs are useful to develop new
CC   ligands with agonistic or antagonistic activity for human TNFalpha
CC   receptor action and are useful in control and prevention of an array of
CC   diseases with (chronic) inflammatory components such as Crohn's disease
CC   and other intestinal ulcerations or irritations. The present sequence
CC   represents a TNFalpha receptor binding peptide which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 24;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          1 LNRRA 5


RESULT 12
ADA19836
ID   ADA19836 standard; peptide; 16 AA.
XX
AC   ADA19836;
XX
DT   20-NOV-2003  (first entry)
XX
DE   TNFalpha receptor binding peptide SEQ ID NO:10.
XX
KW   molecular library; identification; detection; binding site;
KW   tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW   protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW   TNFalpha receptor; tumour necrosis factor alpha receptor;
KW   inflammatory disease; Crohn's disease; intestinal ulceration;
KW   intestinal irritation.
XX
OS   Synthetic.
XX
PN   EP1279962-A1.
XX
PD   29-JAN-2003.
XX
PF   27-JUL-2001; 2001EP-00202879.
XX
PR   27-JUL-2001; 2001EP-00202879.
XX
PA   (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI   Slootstra JW,  Puijk WC,  Van Dijk E;
XX
DR   WPI; 2003-259178/26.
XX
PT   Producing molecular library for identifying binding site of tumor
PT   necrosis factor-alpha, comprises providing the library with many
PT   molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS   Disclosure; Page 16; 70pp; English.
XX
CC   The present invention describes a method (M1) for producing a molecular
CC   library for identifying or detecting a binding site of tumour necrosis
CC   factor alpha (TNFalpha). (M1) comprises providing the library with
CC   several molecules, and further generating at least one of the molecules
CC   by linking a first segment to a second segment. Also described: (1) a
CC   library (I) comprising several molecules comprising at least a first and
CC   a second segment obtainable by (M1); (2) a solid support (II) comprising
```

CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 1 LNRRA 5

RESULT 13
ABR42094
ID ABR42094 standard; peptide; 17 AA.
XX
AC ABR42094;
XX
DT 28-JUL-2003 (first entry)
XX
DE Human tumour necrosis factor-alpha external surface loop AA.
XX
KW Human; tumour necrosis factor-alpha; RANKL; osteopathic; bone.
XX
OS Homo sapiens.
XX
PN WO2003033663-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033022.
XX
PR 15-OCT-2001; 2001US-0329393P.
XX
PA (BARN-) BARNES-JEWISH HOSPITAL.
XX
PI Lam J, Ross PF, Teitelbaum SL;
XX
DR WPI; 2003-430346/40.
XX
PT New RANKL mimic comprising a core, and at least one external loop, useful
PT for enhancing processes of bone formation or inhibiting bone resorption,
PT thus providing treatments for disease or condition characterized by loss
PT of bone mass.
XX
PS Disclosure; Page 15; 78pp; English.
XX
CC The present sequence is that of the AA" external surface loop of human
CC tumour necrosis factor (TNF)-alpha. The invention provides non-naturally-
CC occurring proteins that contain one or more of the external surface loops
CC of RANKL in combination with a heterologous protein core obtained from a
CC non-RANKL member of the TNF superfamily. Thus, the present external loop
CC sequence is replaceable by a RANKL external loop sequence. Such proteins
CC bind to RANK, acting as mimics of RANKL, and can be used to enhance bone
CC formation by either inhibiting bone resorption or inducing osteogenesis,
CC thus providing treatments for diseases or conditions characterised by
CC loss of bone mass
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 24; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 11 LNRRA 15

RESULT 14
AAR05522
ID AAR05522 standard; protein; 20 AA.
XX
AC AAR05522;
XX
DT 25-MAR-2003 (revised)
DT 24-OCT-1990 (first entry)
XX
DE Tumour necrosis factor derived peptide.
XX
KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease;
KW infection; inflammation; transplant rejection.
XX
OS Synthetic.
XX
PN DE3841767-A.
XX
PD 13-JUN-1990.
XX
PF 12-DEC-1988; 88DE-03841767.
XX
PR 12-DEC-1988; 88DE-03841767.
XX
PA (BADI) BASF AG.
PA (BOEH/) BOEHM H J.
XX
PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
XX
DR WPI; 1990-186583/25.
XX
PT Peptide tumour necrosis factor analogues - used in treatment of tumours
PT and auto:immune diseases.
XX
PS Example 16; Page 8; 16pp; German.
XX
CC To residue V1 is attached AcH and to residue A20 NH2. This peptide is an
CC example of a highly generic sequence of the formula X-A-B-E-Leu-Y A= Glu,
CC Pro or Gln; B= Gly, Glu, Asn or Asp; E= Gln or Ser; X= G-NH-CHM-CO, G-NH-
CC CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH-CHQ-COZ, V-NH-CHQ-
CC COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or a protecting group; Z= OH,
CC NH2 or carboxy protecting group; or G and Z together are a covalent bond
CC or the gp. CO(CH2)aNH; a=1-12; R and U= peptide chains of 1-5 naturally
CC occuring alpha aminoacids; W= one of the following dodecapeptide chains:
CC kpvahvvanpqa, kpvahvvadins, kplahvvanpqv, kpvahvvanhqv, kpaahligdpsk,
CC kpaahlvgdpst, kpaahlvgypsk. or a partial sequence of 5-11 amino acids
CC from one of the chains, or a peptide chain of 1-4 naturally occurring
CC alpha amino acids; V= one of the following dodecapeptide chains:

CC qwlnrranalla, rwwdsyanalma, qwlsqranalla, ewlsqranalla, lwrantdraflq,
CC rwrantdraflr, lwrastdraflr. or a partial sequence of 5-11 amino acids
CC from one of the chains, or a peptide chain of 1-4 natural alpha amino
CC acids; M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxyethyl, 3-
CC indolyl, 4-imidazoly-methyl or (CH2)bT; b=1-6; T= OH, MeO, MeS,
CC isopropyl, phenyl (opt. 4-OH, substd), mercapto, amino, carboxy,
CC carbamoyl or quanidino; or M ans Q together are (CH2)c-S-S-(CH2)d,
CC (CH2)eCO NH-(CH2)f or (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and
CC f=1-6; g=1-12. The peptide is a low mol. wt. deriv. of TNF. See also
CC DE3841753-55, DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 24; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||| |
Db 14 LNRRA 18

RESULT 15
AAR06807
ID AAR06807 standard; protein; 21 AA.
XX
AC AAR06807;
XX
DT 25-MAR-2003 (revised)
DT 24-OCT-1990 (first entry)
XX
DE Tumour necrosis factor derived peptide.
XX
KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease;
KW infection; inflammation; transplant rejection; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 21. .21
FT /label= OTHER
FT /note= "Ahx"
XX
PN DE3841767-A.
XX
PD 13-JUN-1990.
XX
PF 12-DEC-1988; 88DE-03841767.
XX
PR 12-DEC-1988; 88DE-03841767.
XX
PA (BADI) BASF AG.
PA (BOEH/) BOEHM H J.
XX
PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
XX
DR WPI; 1990-186583/25.
XX
PT Peptide tumour necrosis factor analogues - used in treatment of tumours
PT and auto:immune diseases.
XX
PS Example 59; Page 13; 16pp; German.
XX
CC This peptide is an example of a highly generic sequence of the formula X-
CC A-B-E-Leu-Y A= Glu, Pro or Gln; B= Gly, Glu, Asn or Asp; E= Gln or Ser;
CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH
CC -CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or a
CC protecting group; Z= OH, NH2 or carboxy protecting group; or G and Z
CC together are a covalent bond or the gp. CO(CH2)aNH; a=1-12; R and U=
CC peptide chains of 1-5 naturally occuring alpha aminoacids; W= one of the
CC following dodecapeptide chains: kpvahvvanpqa, kpvahvvadins, kplahvvanpqv,
CC kpvahvvanhqv, kpaahligdpsk, kpaahlvgdpst, kpaahlvgypsk. or a partial
CC sequence of 5-11 amino acids from one of the chains, or a peptide chain
CC of 1-4 naturally occurring alpha amino acids; V= one of the following
CC dodecapeptide chains: qwlnrranalla, rwwdsyanalma, qwlsqranalla,
CC ewlsqranalla, lwrantdraflq, rwrantdraflr, lwrastdraflr. or a partial
CC sequence of 5-11 amino acids from one of the chains, or a peptide chain
CC of 1-4 natural alpha amino acids; M and Q= H, isopropyl, sec-butyl,
CC phenyl, 1-hydroxyethyl, 3-indolyl 4-imidazoly-methyl or (CH2)bT; b=1-6;
CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto, amino,
CC carboxy, carbamoyl or quanidino; or M ans Q together are (CH2)c-S-S-
CC (CH2)d, (CH2)eCO NH-(CH2)f or (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4;
CC e and f=1-6; g=1-12. The peptide is a low mol. wt. deriv. of TNF. See
CC also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-
CC MAR-2003 to correct PA field.)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 24; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||| |
Db 14 LNRRA 18

Search completed: February 16, 2005, 20:32:21
Job time : 136 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 16, 2005, 20:32:38 ; Search time 14 Seconds
(without alignments)
14.044 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 154980 seqs, 39324206 residues

Total number of hits satisfying chosen parameters: 154980

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	154	6	US-10-450-763-41187	Sequence 41187, A
2	24	100.0	157	5	US-09-920-137C-9	Sequence 9, Appli
3	24	100.0	157	7	US-11-021-951-96	Sequence 96, Appl
4	24	100.0	166	6	US-10-916-286A-114	Sequence 114, App
5	24	100.0	166	6	US-10-916-286A-117	Sequence 117, App
6	24	100.0	189	6	US-10-916-286A-108	Sequence 108, App
7	24	100.0	189	6	US-10-916-286A-111	Sequence 111, App
8	24	100.0	195	6	US-10-489-448-2916	Sequence 2916, Ap
9	24	100.0	205	8	US-60-643-717-3674	Sequence 3674, Ap
10	24	100.0	206	8	US-60-643-717-713	Sequence 713, App
11	24	100.0	233	7	US-11-028-780-4	Sequence 4, Appli
12	24	100.0	233	8	US-60-643-337-4	Sequence 4, Appli
13	24	100.0	280	6	US-10-450-763-35472	Sequence 35472, A
14	24	100.0	285	1	PCT-IB03-06509-1779	Sequence 1779, Ap
15	24	100.0	296	1	PCT-IB03-06509-3796	Sequence 3796, Ap
16	24	100.0	345	7	US-11-031-175-12894	Sequence 12894, A
17	24	100.0	353	7	US-11-031-175-15109	Sequence 15109, A
18	24	100.0	391	8	US-60-643-717-3773	Sequence 3773, Ap
19	24	100.0	504	7	US-11-031-175-10955	Sequence 10955, A
20	24	100.0	586	6	US-10-450-763-43413	Sequence 43413, A
21	24	100.0	637	6	US-10-450-763-49376	Sequence 49376, A
22	24	100.0	639	6	US-10-450-763-51849	Sequence 51849, A
23	24	100.0	700	7	US-11-031-175-11256	Sequence 11256, A
24	24	100.0	964	7	US-11-031-175-14068	Sequence 14068, A
25	24	100.0	978	7	US-11-031-175-13903	Sequence 13903, A
26	24	100.0	1460	6	US-10-450-763-43666	Sequence 43666, A
27	24	100.0	1735	7	US-11-031-175-14547	Sequence 14547, A
28	22	91.7	153	6	US-10-489-448-1000	Sequence 1000, Ap
29	22	91.7	414	8	US-60-643-717-2857	Sequence 2857, Ap
30	22	91.7	756	6	US-10-450-763-57827	Sequence 57827, A
31	21	87.5	62	6	US-10-450-763-59166	Sequence 59166, A
32	21	87.5	114	6	US-10-450-763-53453	Sequence 53453, A
33	21	87.5	121	7	US-11-031-175-14329	Sequence 14329, A
34	21	87.5	178	6	US-10-450-763-57202	Sequence 57202, A
35	21	87.5	178	8	US-60-643-717-2833	Sequence 2833, Ap
36	21	87.5	179	6	US-10-450-763-35069	Sequence 35069, A
37	21	87.5	185	6	US-10-450-763-30731	Sequence 30731, A
38	21	87.5	206	6	US-10-450-763-48364	Sequence 48364, A
39	21	87.5	208	6	US-10-450-763-47866	Sequence 47866, A
40	21	87.5	267	8	US-60-643-717-7767	Sequence 7767, Ap
41	21	87.5	311	7	US-11-027-399-3454	Sequence 3454, Ap
42	21	87.5	311	7	US-11-027-843-3454	Sequence 3454, Ap
43	21	87.5	311	7	US-11-027-878-3454	Sequence 3454, Ap
44	21	87.5	311	7	US-11-028-169-3454	Sequence 3454, Ap
45	21	87.5	311	7	US-11-028-204-3454	Sequence 3454, Ap

ALIGNMENTS

RESULT 1
US-10-450-763-41187
; Sequence 41187, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 41187
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-41187

Query Match 100.0%; Score 24; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LNRRA 5
              |||||
Db         34 LNRRA 38
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RESULT 2
US-09-920-137C-9
; Sequence 9, Application US/09920137C
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallon
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250
; CURRENT APPLICATION NUMBER: US/09/920,137C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826

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;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 9
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-920-137C-9

  Query Match           100.0%;  Score 24;  DB 5;  Length 157;
  Best Local Similarity  100.0%;  Pred. No. 43;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         29 LNRRA 33


RESULT 3
US-11-021-951-96
; Sequence 96, Application US/11021951
; GENERAL INFORMATION:
;  APPLICANT: HAUPTS, Ulrich
;  APPLICANT:  KOLTERMANN, Andre
;  APPLICANT:  SCHEIDIG, Andreas
;  APPLICANT:  VOTSMEIER, Christian
;  APPLICANT:  Kettling, Ulrich
;  APPLICANT:  COCO, Wayne Michael
;  TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
;  TITLE OF INVENTION:  And Diagnostic Use Thereof
;  FILE REFERENCE: 04156.0002U5
;  CURRENT APPLICATION NUMBER: US/11/021,951
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: 10/872,198
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 60/543,518
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/524,960
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: EP 04003058
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: EP 03025871
;  PRIOR FILING DATE: 2003-11-11
;  PRIOR APPLICATION NUMBER: EP 03025851
;  PRIOR FILING DATE: 2003-11-10
;  PRIOR APPLICATION NUMBER: EP 03013819
;  PRIOR FILING DATE: 2003-06-18
;  NUMBER OF SEQ ID NOS: 191
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-021-951-96

  Query Match           100.0%;  Score 24;  DB 7;  Length 157;
  Best Local Similarity  100.0%;  Pred. No. 43;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         29 LNRRA 33


RESULT 4
US-10-916-286A-114
; Sequence 114, Application US/10916286A
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT:  Dreitz, Matthew J.
;  TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
;  FILE REFERENCE: IM-2-C1-R
;  CURRENT APPLICATION NUMBER: US/10/916,286A
;  CURRENT FILING DATE:  2004-08-11
;  PRIOR APPLICATION NUMBER: 09/322,409
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,306
;  PRIOR FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Felis catus
US-10-916-286A-114

  Query Match           100.0%;  Score 24;  DB 6;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         10 LNRRA 14


RESULT 5
US-10-916-286A-117
; Sequence 117, Application US/10916286A
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT:  Dreitz, Matthew J.
;  TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
;  FILE REFERENCE: IM-2-C1-R
;  CURRENT APPLICATION NUMBER: US/10/916,286A
;  CURRENT FILING DATE:  2004-08-11
;  PRIOR APPLICATION NUMBER: 09/322,409
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,306
;  PRIOR FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Felis catus
US-10-916-286A-117

  Query Match           100.0%;  Score 24;  DB 6;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         10 LNRRA 14


RESULT 6
US-10-916-286A-108
; Sequence 108, Application US/10916286A
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT:  Dreitz, Matthew J.
;  TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
;  FILE REFERENCE: IM-2-C1-R
;  CURRENT APPLICATION NUMBER: US/10/916,286A
;  CURRENT FILING DATE:  2004-08-11
;  PRIOR APPLICATION NUMBER: 09/322,409
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,306
;  PRIOR FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
;   LENGTH: 189
;   TYPE: PRT
;   ORGANISM: Felis catus
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US-10-916-286A-108

Query Match 100.0%; Score 24; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LNRRA 5
              |||||
Db         33 LNRRA 37
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RESULT 7
US-10-916-286A-111
; Sequence 111, Application US/10916286A
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
; FILE REFERENCE: IM-2-C1-R
; CURRENT APPLICATION NUMBER: US/10/916,286A
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Felis catus
US-10-916-286A-111

Query Match 100.0%; Score 24; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LNRRA 5
              |||||
Db         33 LNRRA 37
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RESULT 8
US-10-489-448-2916
; Sequence 2916, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yunqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 2916
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-2916

Query Match 100.0%; Score 24; DB 6; Length 195;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LNRRA 5
              |||||
Db        158 LNRRA 162
```

RESULT 9
US-60-643-717-3674
; Sequence 3674, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 3674
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Ralstonia eutropha JMP134
US-60-643-717-3674

Query Match 100.0%; Score 24; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LNRRA 5
              |||||
Db        113 LNRRA 117
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RESULT 10
US-60-643-717-713
; Sequence 713, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 713
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Ralstonia metallidurans CH34
US-60-643-717-713

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  Query Match             100.0%;  Score 24;  DB 8;  Length 206;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        115 LNRRA 119


RESULT 11
US-11-028-780-4
; Sequence 4, Application US/11028780
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.,
;  TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
;  FILE REFERENCE: PF559C1
;  CURRENT APPLICATION NUMBER: US/11/028,780
;  CURRENT FILING DATE:  2005-01-05
;  PRIOR APPLICATION NUMBER: 10/202,062
;  PRIOR FILING DATE: 2002-07-25
;  PRIOR APPLICATION NUMBER: 60/307,838
;  PRIOR FILING DATE: 2001-07-27
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: human
US-11-028-780-4

  Query Match             100.0%;  Score 24;  DB 7;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        105 LNRRA 109


RESULT 12
US-60-643-337-4
; Sequence 4, Application US/60643337
; GENERAL INFORMATION:
;  APPLICANT: Rosenblum, Michael
;  TITLE OF INVENTION: Targeted Chimeric Molecules for Cancer Therapy
;  FILE REFERENCE: CLFR:053USP1
;  CURRENT APPLICATION NUMBER: US/60/643,337
;  CURRENT FILING DATE:  2005-01-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Human
US-60-643-337-4

  Query Match             100.0%;  Score 24;  DB 8;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        105 LNRRA 109


RESULT 13
US-10-450-763-35472
; Sequence 35472, Application US/10450763
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 35472
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (7)..(54)
;   OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
;   OTHER INFORMATION: eMATRIX, accession number DM01354V, p-value=1.000e-40, raw score
;   OTHER INFORMATION: 12.97
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(280)
;   OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-35472

  Query Match             100.0%;  Score 24;  DB 6;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        137 LNRRA 141


RESULT 14
PCT-IB03-06509-1779
; Sequence 1779, Application PC/TIB0306509
; GENERAL INFORMATION:
;  APPLICANT: Regents of the University of Minnesota and The United States of America
;  APPLICANT:  Secretary of Agriculture
;  TITLE OF INVENTION: Mycobacterial Diagnostics
;  FILE REFERENCE: 09531/112WO1
;  CURRENT APPLICATION NUMBER: PCT/IB03/06509
;  CURRENT FILING DATE:  2003-03-06
;  PRIOR APPLICATION NUMBER: 10/137,113
;  PRIOR FILING DATE: 2002-04-30
;  PRIOR APPLICATION NUMBER: 60/362,396
;  PRIOR FILING DATE: 2002-03-06
;  NUMBER OF SEQ ID NOS: 5809
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1779
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Mycobacterium paratuberculosis
PCT-IB03-06509-1779

  Query Match             100.0%;  Score 24;  DB 1;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         55 LNRRA 59


RESULT 15
PCT-IB03-06509-3796
; Sequence 3796, Application PC/TIB0306509
; GENERAL INFORMATION:
;  APPLICANT: Regents of the University of Minnesota and The United States of America
;  APPLICANT:  Secretary of Agriculture
;  TITLE OF INVENTION: Mycobacterial Diagnostics
;  FILE REFERENCE: 09531/112WO1
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;  CURRENT APPLICATION NUMBER: PCT/IB03/06509
;  CURRENT FILING DATE:  2003-03-06
;  PRIOR APPLICATION NUMBER: 10/137,113
;  PRIOR FILING DATE: 2002-04-30
;  PRIOR APPLICATION NUMBER: 60/362,396
;  PRIOR FILING DATE: 2002-03-06
;  NUMBER OF SEQ ID NOS: 5809
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3796
;   LENGTH: 296
;   TYPE: PRT
;   ORGANISM: Mycobacterium paratuberculosis
PCT-IB03-06509-3796

  Query Match            100.0%;  Score 24;  DB 1;  Length 296;
  Best Local Similarity  100.0%;  Pred. No. 90;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        186 LNRRA 190


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GenCore version 5.1.6

OM protein - protein search, using sw model

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Title: US-10-716-030-1
Perfect score: 24
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	60	2	S43777	hypothetical prote
2	24	100.0	122	2	E69980	hypothetical prote
3	24	100.0	144	2	H82837	conserved hypothet
4	24	100.0	189	2	S04670	hypothetical prote
5	24	100.0	194	2	JS0664	interferon precurs
6	24	100.0	233	1	QWHUN	tumor necrosis fac
7	24	100.0	233	1	S22052	tumor necrosis fac
8	24	100.0	237	2	C87656	GGDEF family prote
9	24	100.0	247	2	E87283	tRNA pseudouridine
10	24	100.0	255	2	AG3435	guanylate kinase (
11	24	100.0	259	2	G95890	probable transcrip
12	24	100.0	278	2	S77601	hypothetical prote
13	24	100.0	285	2	I38248	steroidogenic acut
14	24	100.0	285	2	JC4315	steroidogenic acut
15	24	100.0	287	2	F70788	hypothetical prote
16	24	100.0	299	1	XREBT	ATP phosphoribosyl
17	24	100.0	299	1	XREC	ATP phosphoribosyl
18	24	100.0	299	2	AC0764	ATP phosphoribosyl
19	24	100.0	299	2	D90981	ATP phosphoribosyl
20	24	100.0	299	2	B85827	ATP phosphoribosyl
21	24	100.0	299	2	AI0188	ATP phosphoribosyl
22	24	100.0	304	2	AI3285	geranyltranstransf
23	24	100.0	306	2	AC2649	ABC transporter, m
24	24	100.0	310	2	I46987	bone sialoprotein
25	24	100.0	319	2	I60446	Shiga-like cytotox
26	24	100.0	325	2	D37476	fiber - human aden
27	24	100.0	337	2	B97431	alpha-glucosides t
28	24	100.0	338	2	T36307	hypothetical prote
29	24	100.0	341	2	T46153	hypothetical prote
30	24	100.0	343	2	T50179	yeast bud pattern
31	24	100.0	362	2	JC5386	steroidogenic acut
32	24	100.0	386	2	B75516	conserved hypothet
33	24	100.0	398	2	E70621	probable argG prot
34	24	100.0	399	2	F87085	arginosuccinate sy
35	24	100.0	415	2	C84698	hypothetical prote
36	24	100.0	430	2	AI2624	hypothetical prote
37	24	100.0	430	2	H97406	hypothetical prote
38	24	100.0	434	2	T50800	hypothetical prote
39	24	100.0	439	2	A42289	glucose-fructose o
40	24	100.0	443	2	B82209	GGDEF family prote
41	24	100.0	453	2	T15374	hypothetical prote
42	24	100.0	461	2	AC0005	probable membrane
43	24	100.0	463	2	AC0969	probable purine pe
44	24	100.0	463	2	C86042	probable transport
45	24	100.0	463	2	B91195	probable transport

ALIGNMENTS

RESULT 1
S43777
hypothetical protein 3 - Synechococcus sp.
C;Species: Synechococcus sp.
C;Date: 10-Dec-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S43777; S32640
R;Newman, J.; Mann, N.H.; Carr, N.G.
Plant Mol. Biol. 24, 679-683, 1994
A;Title: Organization and transcription of the class I phycoerythrin genes of the marin
A;Reference number: S43777; MUID:94207193; PMID:7512390
A;Accession: S43777
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <NEW>
A;Cross-references: UNIPROT:Q08090; EMBL:X72961; NID:g288983; PIDN:CAA51463.1; PID:g288
A;Note: the authors translated the codon CAC for residue 27 as His

Query Match 100.0%; Score 24; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 20 LNRRA 24

RESULT 2
E69980
hypothetical protein yrvB - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: E69980
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69980
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-122 <KUN>

A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14725.1; PID:e1184014;
A;Experimental source: strain 168
C;Genetics:
A;Gene: yrvB

Query Match 100.0%; Score 24; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 68 LNRRA 72

RESULT 3
H82837
conserved hypothetical protein XF0184 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82837
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82837
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <SIM>
A;Cross-references: UNIPROT:Q9PGW4; GB:AE003872; GB:AE003849; NID:g9104975; PIDN:AAF8299
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0184

Query Match 100.0%; Score 24; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 84 LNRRA 88

RESULT 4
S04670
hypothetical protein 5 - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S04670
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04670
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-189 <TYB>
A;Cross-references: UNIPROT:P05448

Query Match 100.0%; Score 24; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 5 LNRRA 9

RESULT 5
JS0664
interferon precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JS0664
R;Nakamura, N.; Sudo, T.; Matsuda, S.; Yanai, A.
Biosci. Biotechnol. Biochem. 56, 211-214, 1992
A;Title: Molecular cloning of feline interferon cDNA by direct expression.
A;Reference number: JS0664; MUID:92323151; PMID:1377975
A;Accession: JS0664
A;Molecule type: mRNA
A;Residues: 1-194 <NAK>
A;Cross-references: UNIPROT:P35849
C;Superfamily: interferon alpha
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-194/Product: interferon #status predicted <INT>
F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 33 LNRRA 37

RESULT 6
QWHUN
tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrc
A;Reference number: A93585; MUID:86016093; PMID:2995927
A;Accession: A93585
A;Molecule type: DNA
A;Residues: 1-233 <NED>
A;Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <IRI>
A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to l
A;Reference number: A93351; MUID:85086244; PMID:6392892
A;Accession: A93351
A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelo
R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;

```
Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
A;Accession: A44189
A;Molecule type: mRNA
A;Residues: 1-62,'S',64-233 <WAN>
A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: B61478
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A;Reference number: I53311; MUID:86030296; PMID:3932069
A;Accession: I53311
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <MAR>
A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A;Experimental source: U-937 cells
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
A;Accession: S62610
A;Molecule type: protein
A;Residues: 77-99 <TAK>
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regio
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
A;Cross-references: GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
out detriment to normal cells. It can also act synergistically with interferon gamma to
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely
ut are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

  Query Match             100.0%;  Score 24;  DB 1;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        105 LNRRA 109


RESULT 7
S22052
tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S22052
R;Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
A;Cross-references: UNIPROT:P33620; EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g3816
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

  Query Match             100.0%;  Score 24;  DB 1;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        105 LNRRA 109


RESULT 8
C87656
GGDEF family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87656
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87656
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <STO>
A;Cross-references: UNIPROT:Q9A3B9; GB:AE005673; NID:g13424977; PIDN:AAK25247.1; GSPDB:(
C;Genetics:
A;Gene: CC3285

  Query Match             100.0%;  Score 24;  DB 2;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         92 LNRRA 96


RESULT 9
E87283
tRNA pseudouridine synthase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87283
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
```

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87283
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <STO>
A;Cross-references: UNIPROT:Q9ABF0; GB:AE005673; NID:g13421415; PIDN:AAK22265.1; GSPDB:G
C;Genetics:
A;Gene: CC0278
C;Superfamily: tRNA-pseudouridine synthase I

Query Match 100.0%; Score 24; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 116 LNRRA 120

RESULT 10
AG3435
guanylate kinase (EC 2.7.4.8) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AG3435
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52650.1; PID:g17983473; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1469
A;Map position: I
C;Keywords: phosphotransferase

Query Match 100.0%; Score 24; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 180 LNRRA 184

RESULT 11
G95890
probable transcription regulator protein [imported] - Sinorhizobium meliloti (strain 102
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95890
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <KUR>
A;Cross-references: UNIPROT:Q92WE9; GB:AL591985; PIDN:CAC48791.1; PID:g15140264; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb20405
A;Genome: plasmid

Query Match 100.0%; Score 24; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 82 LNRRA 86

RESULT 12
S77601
hypothetical protein 278 - Paracoccus denitrificans
C;Species: Paracoccus denitrificans
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S77601
R;de Gier, J.W.; Schepper, M.; Reijnders, W.N.M.; van Dyck, S.J.; Slotboom, D.J.; Warne,
Mol. Microbiol. 20, 1247-1260, 1996
A;Title: Structural and functional analysis of aa(3)-type and cbb(3)-type cytochrome c o
A;Reference number: S77595; MUID:96405647; PMID:8809776
A;Accession: S77601
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-278 <DEA>
A;Cross-references: UNIPROT:Q51678; EMBL:U34353; NID:g1002874; PIDN:AAC44515.1; PID:g10
A;Experimental source: strain Pd1222
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995

Query Match 100.0%; Score 24; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 232 LNRRA 236

RESULT 13
I38248
steroidogenic acute regulatory protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38248; I38896
R;Sugawara, T.; Lin, D.; Holt, J.A.; Martin, K.O.; Javitt, N.B.; Miller, W.L.; Strauss,
Biochemistry 34, 12506-12512, 1995
A;Title: Structure of the human steroidogenic acute regulatory protein (StAR) gene: StAR
A;Reference number: I38248; MUID:96038208; PMID:7547998
A;Accession: I38248
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-285 <RES>
A;Cross-references: UNIPROT:P49675; EMBL:U29105; NID:g1041696; PIDN:AAC50234.1; PID:g104
R;Sugawara, T.; Holt, J.A.; Driscoll, D.; Strauss III, J.F.; Lin, D.; Miller, W.L.; Patt
Proc. Natl. Acad. Sci. U.S.A. 92, 4778-4782, 1995
A;Title: Human steroidogenic acute regulatory protein: functional activity in COS-1 cell
A;Reference number: I38896; MUID:95281540; PMID:7761400
A;Accession: I38896
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-285 <RE2>
A;Cross-references: EMBL:U17280; NID:g727252; PIDN:AAC50141.1; PID:g727253
C;Genetics:
A;Gene: StAR
A;Cross-references: GDB:STAR; GDB:635457; OMIM:600617
A;Map position: 8p11.2-8p11.2

A;Introns: 22/1; 60/1; 102/3; 155/3; 217/2; 248/3

Query Match 100.0%; Score 24; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||||
Db 35 LNRRA 39

RESULT 14
JC4315
steroidogenic acute regulatory protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4315
R;Hartung, S.; Rust, W.; Balvers, M.; Ivell, R.
Biochem. Biophys. Res. Commun. 215, 646-653, 1995
A;Title: Molecular cloning and in vivo expression of the bovine steroidogenic acute regu
A;Reference number: JC4315; MUID:96011827; PMID:7488004
A;Accession: JC4315
A;Molecule type: mRNA
A;Residues: 1-285 <HAR>
A;Cross-references: UNIPROT:Q28918
C;Comment: This protein is an acute controller of the rate-limiting transfer ofcholester
C;Genetics:
A;Gene: StAR
F;226-264/Region: metalloproteinase-1 tissue inhibitor similarity

Query Match 100.0%; Score 24; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||||
Db 35 LNRRA 39

RESULT 15
F70788
hypothetical protein Rv3661 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004
C;Accession: F70788
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70788
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-287 <COL>
A;Cross-references: UNIPROT:O69629; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA1798
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3661
C;Superfamily: Conserved hypothetical protein with haloacid dehalogenase-like hydrolase

Query Match 100.0%; Score 24; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||||
Db 55 LNRRA 59

Search completed: February 16, 2005, 20:35:02
Job time : 26.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 16, 2005, 20:16:35 ; Search time 52.5 Seconds
(without alignments)
48.769 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	60	2	Q08090	Q08090 synechococc
2	24	100.0	72	2	Q853W6	Q853w6 mycobacteri
3	24	100.0	97	2	Q8FE20	Q8fe20 escherichia
4	24	100.0	98	2	Q8VUX4	Q8vux4 staphylococ
5	24	100.0	98	2	Q9LBZ5	Q9lbz5 staphylococ
6	24	100.0	98	2	Q6GD55	Q6gd55 staphylococ
7	24	100.0	100	1	HIS1_KLEPN	P05148 klebsiella
8	24	100.0	110	2	Q9F5L4	Q9f514 bradyrhizob
9	24	100.0	114	2	Q6F4B4	Q6f4b4 trachemys s
10	24	100.0	117	2	Q9P071	Q9p071 homo sapien
11	24	100.0	121	2	Q71I70	Q71i70 lactobacill
12	24	100.0	124	2	Q6F4B3	Q6f4b3 trachemys s
13	24	100.0	138	2	Q9TTG7	Q9ttg7 aotus lemur
14	24	100.0	139	2	Q7XYL8	Q7xyl8 chlorarachn
15	24	100.0	139	2	Q7NFX2	Q7nfx2 gloeobacter
16	24	100.0	144	2	Q8P6T7	Q8p6t7 xanthomonas
17	24	100.0	144	2	Q87EZ5	Q87ez5 xylella fas
18	24	100.0	144	2	Q9PGW4	Q9pgw4 xylella fas
19	24	100.0	145	2	Q6IWS7	Q6iws7 burkholderi
20	24	100.0	148	2	Q8SWQ2	Q8swq2 encephalito
21	24	100.0	149	2	O97538	O97538 aotus vocif
22	24	100.0	149	2	O97543	O97543 aotus nancy
23	24	100.0	149	2	Q9TTG8	Q9ttg8 aotus nigri
24	24	100.0	150	2	Q8LRS2	Q8lrs2 sorbus aucu
25	24	100.0	155	2	Q8HZD5	Q8hzd5 saguinus oe
26	24	100.0	155	2	Q8HZD7	Q8hzd7 pongo pygma
27	24	100.0	155	2	Q8HZD8	Q8hzd8 gorilla gor
28	24	100.0	158	2	Q6MM44	Q6mm44 bdellovibri
29	24	100.0	169	2	Q6DQL8	Q6dql8 zea mays (m
30	24	100.0	173	2	Q6F9C6	Q6f9c6 acinetobact
31	24	100.0	179	2	Q7XJ85	Q7xj85 pyrus commu
32	24	100.0	182	2	Q6MGM4	Q6mgm4 bdellovibri
33	24	100.0	186	2	Q7Q4A8	Q7q4a8 anopheles g
34	24	100.0	188	2	Q863I5	Q863i5 felis silve
35	24	100.0	188	2	Q863I6	Q863i6 felis silve
36	24	100.0	189	1	YAT5_RHOBL	P05448 rhodopseudo
37	24	100.0	189	2	Q8MIL3	Q8mil3 felis silve
38	24	100.0	189	2	Q8MIL4	Q8mil4 felis silve
39	24	100.0	189	2	Q8MIL5	Q8mil5 felis silve
40	24	100.0	189	2	Q8MIL7	Q8mil7 felis silve
41	24	100.0	189	2	Q863I7	Q863i7 felis silve
42	24	100.0	189	2	Q863I8	Q863i8 felis silve
43	24	100.0	189	2	Q863I9	Q863i9 felis silve
44	24	100.0	189	2	Q863J0	Q863j0 felis silve
45	24	100.0	194	1	INA_FELCA	P35849 felis silve

ALIGNMENTS

RESULT 1
Q08090
ID Q08090 PRELIMINARY; PRT; 60 AA.
AC Q08090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CpeB, cpeA genes and ORF3 (Fragment).
OS Synechococcus sp.
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1131;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94207193; PubMed=7512390;
RA Newman J., Mann N.H., Carr N.G.;
RT "Organization and transcription of the class I phycoerythrin genes of
RT the marine cyanobacterium Synechococcus sp. WH7803.";
RL Plant Mol. Biol. 24:679-683(1994).
DR EMBL; X72961; CAA51463.1; -.
DR PIR; S43777; S43777.
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6678 MW; 8773BCE2E82BECAC CRC64;

Query Match 100.0%; Score 24; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 20 LNRRA 24

RESULT 2
Q853W6
ID Q853W6 PRELIMINARY; PRT; 72 AA.
AC Q853W6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp200.
GN Name=200;
OS Mycobacteriophage Omega.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).

```
DR   EMBL; AY129338; AAN12842.1; -.
SQ   SEQUENCE   72 AA;  8042 MW;  A38DAC1C5529B6F1 CRC64;

  Query Match           100.0%;  Score 24;  DB 2;  Length 72;
  Best Local Similarity  100.0%;  Pred. No. 84;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         16 LNRRA 20


RESULT 3
Q8FE20
ID   Q8FE20      PRELIMINARY;      PRT;    97 AA.
AC   Q8FE20;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein c3549.
GN   OrderedLocusNames=c3549;
OS   Escherichia coli O6.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=217992;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX   MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA   Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA   Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA   Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA   Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT   "Extensive mosaic structure revealed by the complete genome sequence
RT   of uropathogenic Escherichia coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR   EMBL; AE016766; AAN81997.1; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   97 AA;  10945 MW;  138BDBF80ACF67E5 CRC64;

  Query Match           100.0%;  Score 24;  DB 2;  Length 97;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         91 LNRRA 95


RESULT 4
Q8VUX4
ID   Q8VUX4      PRELIMINARY;      PRT;    98 AA.
AC   Q8VUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ORF12.
OS   Staphylococcus hominis.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1290;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GIFU12263;
RX   MEDLINE=22586405; PubMed=12700250;
RX   DOI=10.1128/JB.185.9.2711-2722.2003;
RA   Katayama Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,
RA   Kobayashi I., Hiramatsu K.;
RT   "Identification in methicillin-susceptible Staphylococcus hominis of
RT   an active primordial mobile genetic element for the staphylococcal
RT   cassette chromosome mec of methicillin-resistant Staphylococcus
RT   aureus.";
RL   J. Bacteriol. 185:2711-2722(2003).
DR   EMBL; AB063171; BAB83483.1; -.
DR   GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.
DR   GO; GO:0006281; P:DNA repair; IEA.
DR   Pfam; PF07205; DUF1413; 1.
SQ   SEQUENCE   98 AA;  11104 MW;  2B95AB85279039C9 CRC64;

  Query Match           100.0%;  Score 24;  DB 2;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         34 LNRRA 38


RESULT 5
Q9LBZ5
ID   Q9LBZ5      PRELIMINARY;      PRT;    98 AA.
AC   Q9LBZ5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCTC10442;
RX   MEDLINE=21199321; PubMed=11302791;
RA   Ito T., Katayama Y., Asada k., Mori N., Tsutsumimoto K.;
RT   "Structural comparison of three types of staphylococcal cassette
RT   chromosome mec integrated in the chromosome in methicillin-resistant
RT   Staphylococcus aureus.";
RL   Antimicrob. Agents Chemother. 45:1323-1336(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCTC10442;
RA   Ito T., Okuma K., Xue M.X., Yuzawa H., Hiramatsu K.;
RT   "Insights on antibiotic resistance of Staphylococcus aureus from its
RT   whole genome: genomic island SCC.";
RL   Drug Resist. Updat. 6:41-52(2003).
DR   EMBL; AB033763; BAA94325.1; -.
DR   GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.
DR   GO; GO:0006281; P:DNA repair; IEA.
DR   InterPro; IPR010813; DUF1413.
DR   InterPro; IPR001497; Methyltransf_1.
DR   Pfam; PF07205; DUF1413; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   98 AA;  11149 MW;  DCCF9E59FFF8AE0A CRC64;

  Query Match           100.0%;  Score 24;  DB 2;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         34 LNRRA 38


RESULT 6
Q6GD55
ID   Q6GD55      PRELIMINARY;      PRT;    98 AA.
AC   Q6GD55;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=SAS0035;
OS   Staphylococcus aureus (strain MSSA476).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=282459;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA   Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA   Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA   Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA   Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA   Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA   James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA   Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
RA   Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA   Spratt B.G., Parkhill J.;
RT   "Complete genomes of two clinical Staphylococcus aureus strains:
RT   evidence for the rapid evolution of virulence and drug resistance.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR   EMBL; BX571857; CAG41807.1; -.
DR   GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.
DR   GO; GO:0006281; P:DNA repair; IEA.
DR   InterPro; IPR010813; DUF1413.
DR   InterPro; IPR001497; Methyltransf_1.
DR   Pfam; PF07205; DUF1413; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   98 AA;  11109 MW;  8D5577B576DE82C6 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         34 LNRRA 38


RESULT 7
HIS1_KLEPN
ID   HIS1_KLEPN     STANDARD;      PRT;   100 AA.
AC   P05148;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ATP phosphoribosyltransferase (EC 2.4.2.17) (ATP-PRTase) (ATP-PRT)
DE   (Fragment).
GN   Name=hisG;
OS   Klebsiella pneumoniae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Klebsiella.
OX   NCBI_TaxID=573;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84135578; PubMed=6321433;
RA   Rodriguez R.L., West R.W. Jr.;
RT   "Histidine operon control region of Klebsiella pneumoniae: analysis
RT   with an Escherichia coli promoter-probe plasmid vector.";
RL   J. Bacteriol. 157:764-771(1984).
CC   -!- FUNCTION: Catalyzes the condensation of ATP and PRPP to form N'-
CC       5'-phosphoribosyl-ATP (PR-ATP). Has a crucial role in the pathway
CC       because the rate of histidine biosynthesis seems to be controlled
CC       primarily by regulation of hisG enzymatic activity (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: 1-(5-phospho-D-ribosyl)-ATP + diphosphate =
CC       ATP + 5-phospho-alpha-D-ribose 1-diphosphate.
CC   -!- COFACTOR: Magnesium (By similarity).
CC   -!- ENZYME REGULATION: Feedback inhibited by histidine (By
CC       similarity).
CC   -!- PATHWAY: Histidine biosynthesis; first step.
CC   -!- SUBUNIT: Equilibrium between an active dimeric form, an inactive
CC       hexameric form and higher aggregates. Interconversion between the
CC       various forms is largely reversible and is influenced by the
CC       natural substrates and inhibitors of the enzyme (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the ATP phosphoribosyltransferase family.
CC       Long subfamily.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; K01997; AAA25073.1; -.
DR   HAMAP; MF_00079; -; 1.
DR   InterPro; IPR001348; ATP_phspho_trans.
DR   Pfam; PF01634; HisG; 1.
DR   PROSITE; PS01316; ATP_P_PHORIBOSYLTR; PARTIAL.
KW   Glycosyltransferase; Histidine biosynthesis; Magnesium; Metal-binding;
KW   Transferase.
FT   NON_TER     100    100
SQ   SEQUENCE   100 AA;  11408 MW;  BDA8FEB042E012DE CRC64;

  Query Match             100.0%;  Score 24;  DB 1;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         82 LNRRA 86


RESULT 8
Q9F5L4
ID   Q9F5L4      PRELIMINARY;      PRT;   110 AA.
AC   Q9F5L4; Q79U54;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   NapD (Periplasmic nitrate reductase).
GN   Name=napD; OrderedLocusNames=blr7037;
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=110spc4;
RX   PubMed=14663073; DOI=10.1099/mic.0.26620-0;
RA   Delgado M., Bonnard N., Tresierra-Ayala A., Bedmar E.J., Muller P.;
RT   "The Bradyrhizobium japonicum napEDABC genes encoding the periplasmic
RT   nitrate reductase are essential for nitrate respiration.";
RL   Microbiology 149:3395-3403(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=110spc4;
RA   Mueller P.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA110;
RX   MEDLINE=22484998; PubMed=12597275;
RA   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA   Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA   Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA   Tabata S.;
RT   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT   Bradyrhizobium japonicum USDA110.";
RL   DNA Res. 9:189-197(2002).
DR   EMBL; AF314590; AAG31647.1; -.
DR   EMBL; AP005960; BAC52302.1; -.
DR   InterPro; IPR005623; NapD.
DR   Pfam; PF03927; NapD; 1.
KW   Complete proteome.
SQ   SEQUENCE   110 AA;  11787 MW;  9546CE2C46FC0BDB CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 LNRRA 5
              |||||
Db         12 LNRRA 16
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RESULT 9
Q6F4B4
ID   Q6F4B4      PRELIMINARY;      PRT;   114 AA.
AC   Q6F4B4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Preproghrelin-1 precursor.
OS   Trachemys scripta elegans.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
OX   NCBI_TaxID=31138;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RX   PubMed=15242751; DOI=10.1016/j.ygcen.2004.05.005;
RA   Kaiya H., Sakata I., Kojima M., Hosoda H., Sakai T., Kangawa K.;
RT   "Structural determination and histochemical localization of ghrelin in
RT   the red-eared slider turtle, Trachemys scripta elegans.";
RL   Gen. Comp. Endocrinol. 138:50-57(2004).
DR   EMBL; AB161457; BAD29730.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR   InterPro; IPR005441; Preproghrelin.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24     48       ghrelin.
SQ   SEQUENCE   114 AA;  13300 MW;  07DE5E24BF9DEDF2 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         47 LNRRA 51
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RESULT 10
Q9P071
ID   Q9P071      PRELIMINARY;      PRT;   117 AA.
AC   Q9P071;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HSPC311 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA   Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF161429; AAF28989.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   117 AA;  13276 MW;  246F7F794620AAFF CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         80 LNRRA 84
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RESULT 11
Q71I70
ID   Q71I70      PRELIMINARY;      PRT;   121 AA.
AC   Q71I70;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ATP-dependent clp protease ATP-binding subunit (Fragment).
OS   Lactobacillus delbrueckii (subsp. lactis).
OC   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC   Lactobacillus.
OX   NCBI_TaxID=29397;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 4797;
RA   Langenheim J.F., Ulrich R.L.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF496381; AAQ07067.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   Pfam; PF00004; AAA; 1.
KW   ATP-binding; Protease.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13107 MW;  48EB5B5A58D4E675 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         53 LNRRA 57
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RESULT 12
Q6F4B3
ID   Q6F4B3      PRELIMINARY;      PRT;   124 AA.
AC   Q6F4B3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Preproghrelin-2 precursor.
OS   Trachemys scripta elegans.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
OX   NCBI_TaxID=31138;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RX   PubMed=15242751; DOI=10.1016/j.ygcen.2004.05.005;
RA   Kaiya H., Sakata I., Kojima M., Hosoda H., Sakai T., Kangawa K.;
RT   "Structural determination and histochemical localization of ghrelin in
RT   the red-eared slider turtle, Trachemys scripta elegans.";
RL   Gen. Comp. Endocrinol. 138:50-57(2004).
DR   EMBL; AB161458; BAD29731.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR   GO; GO:0050791; P:regulation of physiological process; IEA.
DR   InterPro; IPR006737; motilin_assoc.
DR   InterPro; IPR005441; Preproghrelin.
DR   Pfam; PF04643; Motilin_assoc; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24     48       ghrelin.
SQ   SEQUENCE   124 AA;  14397 MW;  86F2544AA7F7B5D8 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 124;
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  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         47 LNRRA 51


RESULT 13
Q9TTG7
ID   Q9TTG7      PRELIMINARY;      PRT;   138 AA.
AC   Q9TTG7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus lemurinus (Northern gray-necked night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX   NCBI_TaxID=43147;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
DR   EMBL; AF097329; AAF21304.1; -.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   138 AA;  15269 MW;  29275EE4F4CD5068 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         22 LNRRA 26


RESULT 14
Q7XYL8
ID   Q7XYL8      PRELIMINARY;      PRT;   139 AA.
AC   Q7XYL8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytoene synthase (Fragment).
OS   Chlorarachnion sp. (strain CCMP 621) (Pedinomonas minutissima).
OC   Eukaryota; Cercozoa; Chlorarachniophyceae; Bigelowiella.
OX   NCBI_TaxID=227086;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CCMP 621;
RX   MEDLINE=22709102; PubMed=12777624; DOI=10.1073/pnas.1230951100;
RA   Archibald J.M., Rogers M.B., Toop M., Ishida K., Keeling P.J.;
RT   "Lateral gene transfer and the evolution of plastid-targeted proteins
RT   in the secondary plastid-containing alga Bigelowiella natans.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7678-7683(2003).
DR   EMBL; AY267662; AAP79176.1; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0009058; P:biosynthesis; IEA.
DR   InterPro; IPR002060; Squ/phyt_synthse.
DR   InterPro; IPR008949; Terpenoid_synth.
DR   Pfam; PF00494; SQS_PSY; 1.
DR   PROSITE; PS01045; SQUALEN_PHYTOEN_SYN_2; UNKNOWN_1.
FT   NON_TER       1       1
SQ   SEQUENCE   139 AA;  15984 MW;  E47FD6CA34130B6D CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        112 LNRRA 116


RESULT 15
Q7NFX2
ID   Q7NFX2      PRELIMINARY;      PRT;   139 AA.
AC   Q7NFX2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Gll3402 protein.
GN   OrderedLocusNames=gll3402;
OS   Gloeobacter violaceus.
OC   Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX   NCBI_TaxID=33072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC 7421;
RX   MEDLINE=22977040; PubMed=14621292;
RA   Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA   Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA   Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT   cyanobacterium that lacks thylakoids.";
RL   DNA Res. 10:137-145(2003).
DR   EMBL; AP006580; BAC91343.1; -.
KW   Complete proteome.
SQ   SEQUENCE   139 AA;  15634 MW;  131E2BFE8344F336 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         42 LNRRA 46


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Job time : 55.5 secs
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